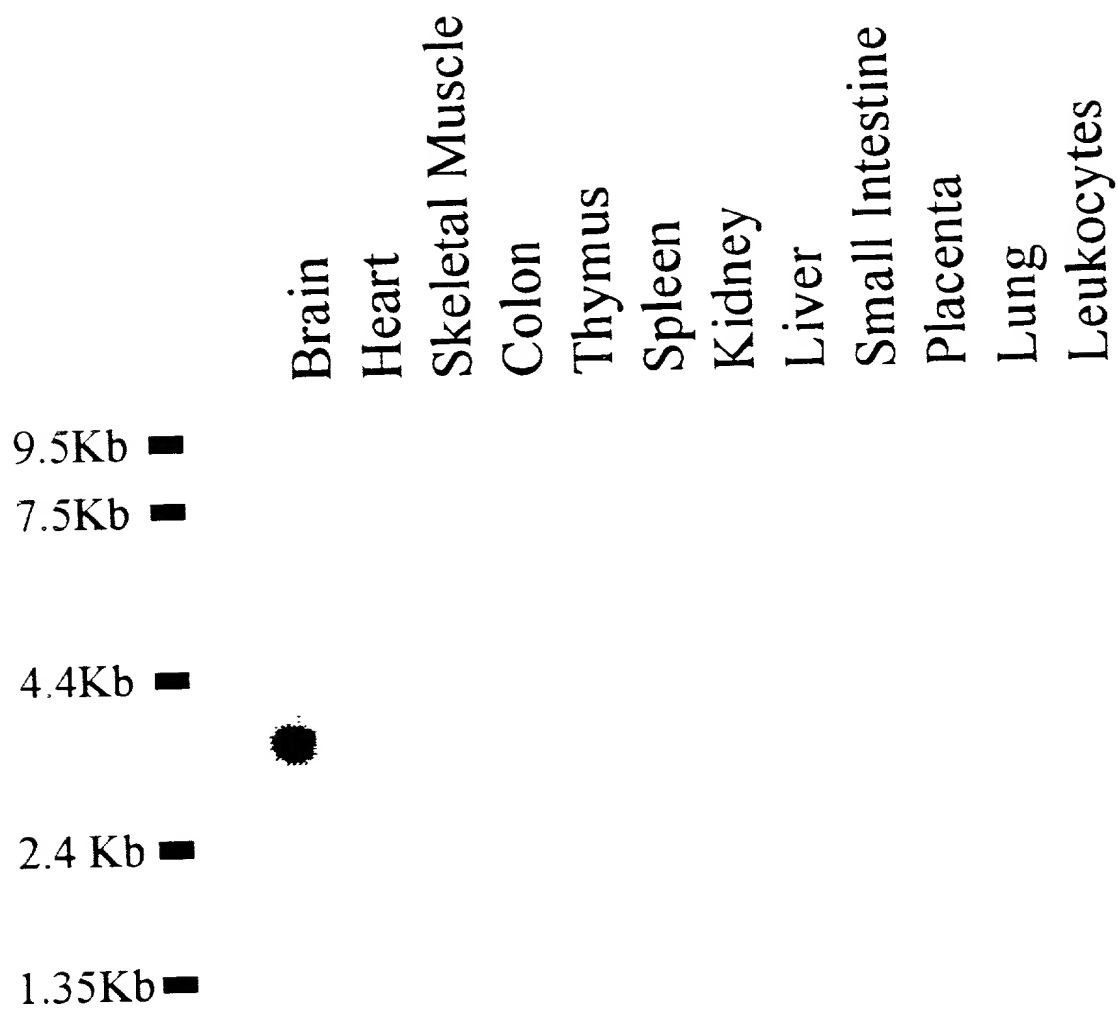


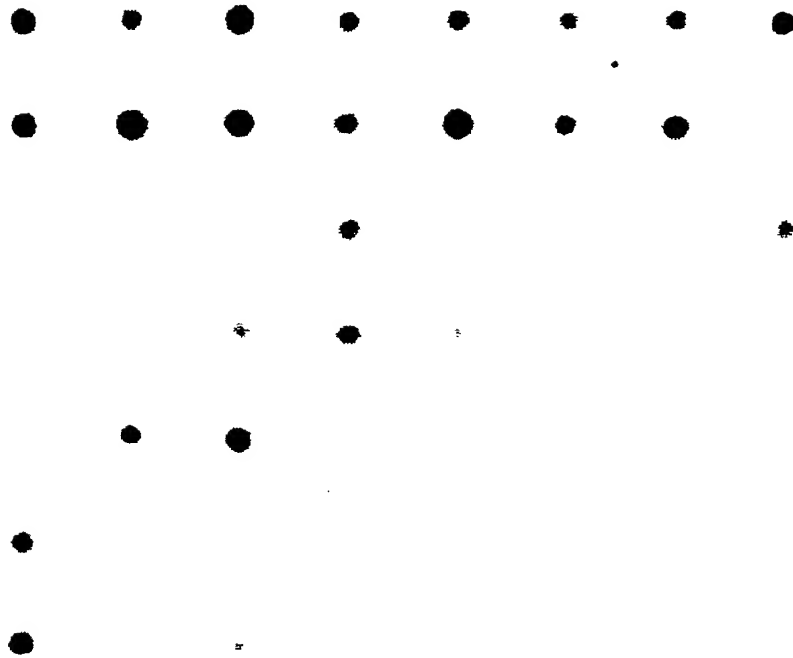
1 MEA---EQRBAAGASEGATPGL EAVPEVAPBPAT-----hHac3.pro
1 -----hHac2.pro
1 MDARGGGGRGESPGATPAEGPPPPPEAPPEGGPGAPPQHPPRAEALPPEAADEGGPRGRhHac1.pro
32 -----AASGP-----hHac3.pro
1 -----hHac2.pro
61 LRSRDSSCGRPGTPGAATAKSPNGECGRGEPQCSPAGPEGPARGPKVSFSCRGAASGP-----hHac1.pro
37 IEKSGP-----EBK-----RRHLGLTLLQPTVKNKFSLRVFGSHKAVEIEQEhHac3.pro
1 -----KEQE-----hHac2.pro
121 AEGPGEAEEAGSEAGPACEPGRGSQASFMQRFQFALLQBGVNKFSLRMFGSQKAVEIEQEhHac1.pro
77 RVKSAGAWIIHPYSDFRYWDLIMLLIMVGNLIIVLPVGITFFKEENSPPWIVFNVLSDTFhHac3.pro
5 RVKTAGFWIIHPYSDFRYWDLIMLLIMVGNLIIVLPVGITFFETITTPWLIIFNVASDTVhHac2.pro
181 RVKSAGAWIIHPYSDFRYWDFTMLLIFMVGNLIIVLPVGITFFKDETAPWIVFNVLSDTFhHac1.pro
137 FLDDLVLNFRGTGIVVEGAETLQAEARARTRYLRTWELVDLSSIPVDYIFLVVELEPRLhHac3.pro
65 FLDDLIMNFRGTGIMNEDSSEIILDEKVIKMNLYLKSFFVVDFFISSIPVDYIFLIVEKG--MhHac2.pro
241 FLDDLVLNFRGTGIVIEDNTEIILDEBEKIKKKYLRTWFFVVDFMSSIPVDYIFLIVEKG--IhHac1.pro
197 DAEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHQWEEIFHMTYDLASAVVRIFNLIGHhac3.pro
123 DSEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHQWEEIFHMTYDLASAVVRIFNLIGHhac2.pro
299 DSEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHQWEEIFHMTYDLASAVMRJCNLLISHhac1.pro
257 MMLLLCHWDFCLQFLVPMLQDFPPDCWVSINHMVNHSWGRQYSHALFKAMSHMLCIGYQQhHac3.pro
183 MMLLLCHWDFCLQFLVPLQLQDFPPDCWVSINEMVNDSWKKQYSYALFKAMSHMLCIGYGAhHac2.pro
359 MMLLLCHWDFCLQFLVPMLQDFPNCWVSINCMVNHSWSELYSFALFKAMSHMLCIGYGRhHac1.pro
317 QAPVGMFDMWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac3.pro
243 QAPVMSDILWLTMLSMIVGATCYAMFVGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac2.pro
419 QAPFSMTDILWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac1.pro

FIG. 1A.

377	PADTRQRIHEIYEYEHRYQGKMFDEESILGEISEPLREEIINFTCRGLVAHMPLEFAHADPSF	hHac3.pro
303	PADMROKIHDIYEYEHRYQGKIIFDEENIINELNDPLREEIVNFCRKLVAITMPLFANADPNF	hHac2.pro
479	PADFROKIHDIYEYEHRYQGKMFDEDSILGELNGPLREEIVNFCRKLVASMPLEFANADPNF	hHac1.pro
437	VTAMLTKLRFEFVQPGDLVVREGSVGRKMYFIZHGLLSVLARGARDTRLTDGSYFGEICL	hHac3.pro
363	VTAMLTKLRFEFVQPGDYIIREGAVGKKMYFIZHGVAGVITKSSKEMKLTDDGSYFGEICL	hHac2.pro
539	VTAMLTKLRFEFVQPGDYIIREGTIGKKMYFIZHGVVSVLTGKNGKEMKLSDDGSYFGEICL	hHac1.pro
497	LTRGRRRTASVRADTYCRLYSLSDVDFHFNALVLEEFPMRRRAFETVAMDRLLRIGKKNSILQR	hHac3.pro
423	LTKGRRRTASVRADTYCRLYSLSDVDNFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIQ	hHac2.pro
599	LTRGRRRTASVRADTYCRLYSLSDVDNFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIH	hHac1.pro
557	R-RSEPSPG--SSGGIMEQHLMQHDRDMARGVGRAPSTGAQLSGKPVLWEPLVHAPLQ	hHac3.pro
483	KFKQKDLNTGVFNNOENETLKQIVKHDREMVQAIAPINYPQMTILNSTSTTTETSRMRTQ	hHac2.pro
459	KVQHDLNLSGVFNNOENALITQELVKVDREMVQQA---ELGQRVGL-----	hHac1.pro
613	AAATTSNVAIALTHQRCPIPLSP-DSPATLTARSAMRSAGSPA--SPLVPVR--AGPW	hHac3.pro
543	SPPVYTATSLSHSNLHSPSPSTQTPQSAILSPCSYTTAVCSPPMQSPIAARTFHYASPT	hHac2.pro
700	-----FPPPPPPPPQVTSATATLQQA-AMSFCEQVARELVGP-LALGSPR	hHac1.pro
666	ASTSRLEAF-PARTLHASLSRAAGRSQVSLGPPPGGG-----GRRIGPR	hHac3.pro
603	ASQLSLMQQQPQQVQSSQPQRQQQH-SPPQPTPGSSTPKNEVHKSTQAIHNTNLTRE	hHac2.pro
743	LVRRPPEGAFAAASPGPFPASPPGAFASPRAPRTSPYGGLPAAPIAGPALPARRLSRA	hHac1.pro
709	GRPLSASQPSLPQRAITCDGSPGRKSGS-ERI-----PPSGILAKPPRTAQPP--	hHac3.pro
662	VRPESAMQPSLPHEVS--TLISRPHPTVGEISIASIPQPVTAVPGTGLQAGGRSTVPQRV	hHac2.pro
803	SRPLSASQPSLPHGAPCPAASPTRPASSTPRLGPTPAARAAPSPDRRDSASPGAAGGL-	hHac1.pro
756	--RPPVPPEATPRGLQLSANM.	hHac3.pro
720	FFRQMSSGAIPENRGVLPAPPLITPHPKK	hHac2.pro
862	-----DEQDSARSLSSNL.	hHac1.pro

FIG. 1B.

*FIG. 2A.*



whole brain	amygdala	caudate nucleus	cere- bellum	cerebral cortex	frontal lobe	hippo- campus	medulla oblongata
occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
appendix	lung	trachea	placenta				
fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	

FIG. 2B.

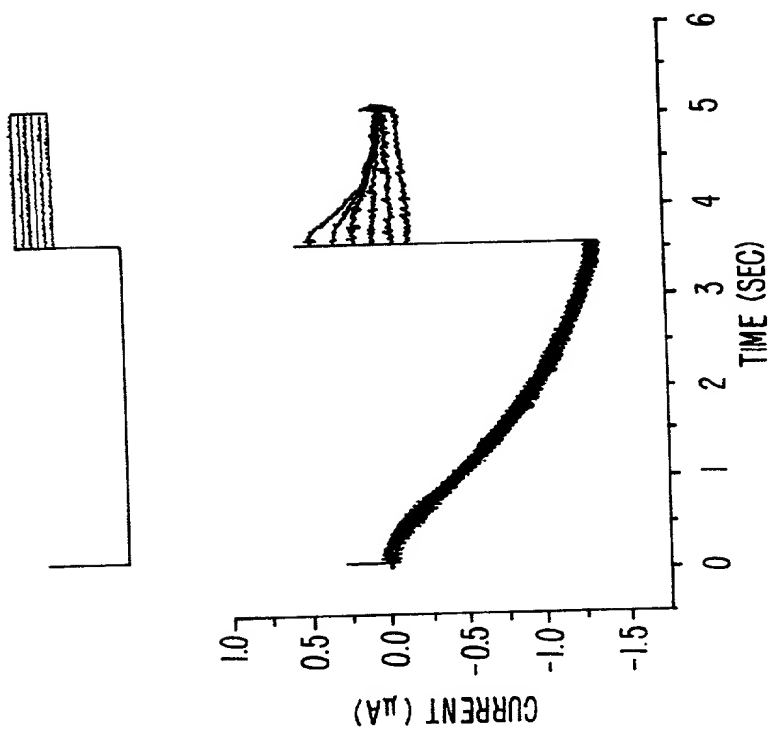


FIG. 3A.

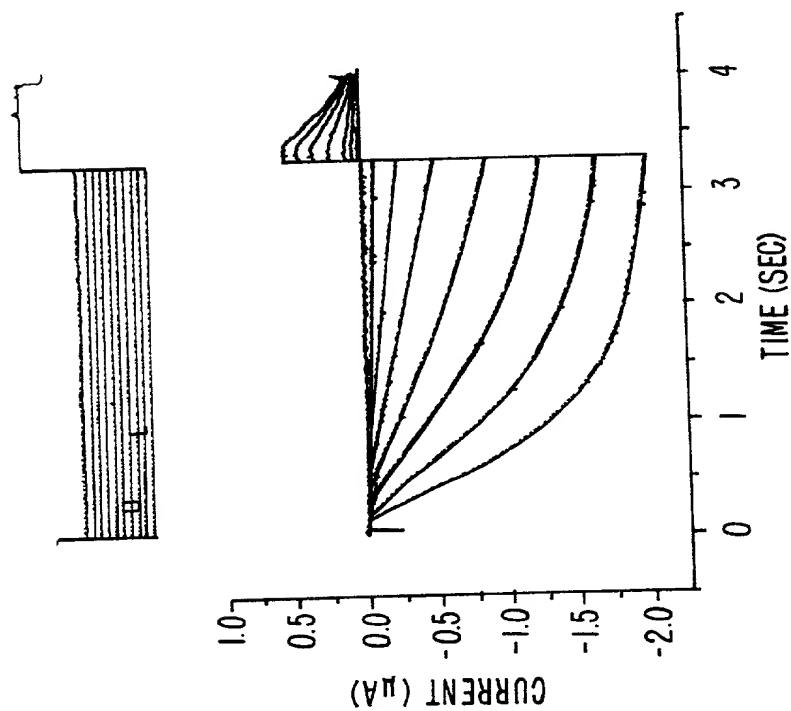
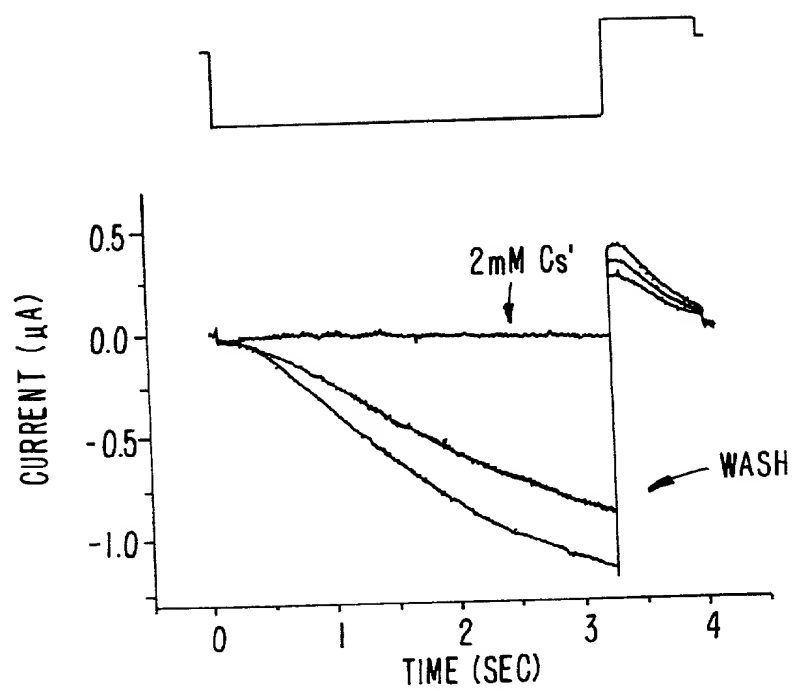


FIG. 3B.

*FIG. 4.*